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Conclusions: In conclusion, synchrotron based FTIR spectroscopy could become a tool to assess tumour cell sensitivity to chemotherapy agents, and to help pathologists in the diagnosis of cancer. We'll discuss here its use as a screening tool to assess the effects of new drugs on cancer cells, and to characterise biomarkers of sensitivity of cancer cells to drugs. Also, we'll discuss here its potential as a screening tool to assess the absence or presence of tumour cells in tissue samples based on spectral biomarkers.

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P2-149 **BSTB: Tumor and Cell Biology Posters, Tue, Sept 4**

Prognostic value of telomerase activity in transthoracic fine-needle biopsy aspirates from non-small cell lung cancer

Targowski, Tomasz[1] Jahnz-Rozyk, Karina[1] Szkoda, Tomasz[2] Qandil, Naim[3] From, Slawomir[1] Plusa, Tadeusz[1]

[1] Military Institute of Health Service, Warsaw, Poland [2] National Institute of Hygiene, Warsaw, Poland [3] Mazovian Center of Lung Diseases and Tuberculosis, Otwock, Poland

Introduction: Non-small cell lung cancer (NSCLC) is the most frequent malignant disease of the respiratory system. Due to an insidious onset and early distant dissemination of NSCLC, results of treatment of even locally non-advanced stages of the disease are highly unsatisfactory. Telomerase activity could be one of prognostic factors, not related to the clinical advancement of cancer.

The Aim of the Study: Evaluation of the relationship between telomerase activity in transthoracic fine-needle biopsy (TFNB) aspirates taken from peripheral NSCLC, cancer advancement, risk of death and survival free of cancer recurrence.

Material and Methods: The study group consisted of 88 patients with peripheral infiltration of the lung. All of them had TFNB of the focal lesion performed. Aspirates were subjected to standard cytological evaluation. Additionally, telomerase activity in the specimens was determined with the PCR-ELISAPLUS method. NSCLC advancement was assessed according to the WHO criteria. The manner of cancer treatment and patient survival were assessed.

Results: NSCLC was newly diagnosed in 79 subjects: 20 patients (25.3%) with stage I, 15 (19.0%) with stage II, 22 (27.85%) with stage III, and 22 (27.85%) with stage IV. In 9 cases, a benign lesion of the lung parenchyma was recognized. An increased telomerase activity was observed in 10 (50%) patients with stage I, in 8 (53%) patients with stage II, in 16 (73%) patients with stage III and 22 (100%) patients with stage IV. Nobody with benign infiltration had a detectable level of telomerase. It was revealed (log-linear analysis) that the higher telomerase activity in primary tumor, the more probable non-operable NSCLC and cancer metastases to distant organs. An increased telomerase activity in TFNB aspirates was related to 7 times higher relative risk of death during the study [RR = 6.9 (CI: 1.8-26.8); $p < 0.05$]. NSCLC recurrence after radical treatment appeared only in 1 (6.2%) case without an increased telomerase activity in comparison to 6 (20%) cases with a detectable telomerase level [RR = 2.5 (CI: 0.3-19.3); $p < 0.05$]. Telomerase activity in aspirates derived from TFNB of peripheral NSCLC could be a helpful independent significant prognostic factor of lung cancer advancement and risk of death or cancer recurrence.

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Marked decline of TARSH gene expression in primary lung cancer

Terauchi, Kunihiko[1] Shimada, Junichi[1] Uekawa, Natsuko[2] Ito, Kazuhiro[1] Yanada, Masashi[1] Shimomura, Masanori[1] Yaoi, Takeshi[3] Maruyama, Mitsuo[2] Fushiki, Shinji[3]

[1] Department of Cardiovascular and Thoracic Surgery, Graduate School of Medical Science, Kyoto Prefectural University of Medicine, Kyoto, Japan [2] Department of Mechanism of Ageing, National Institute for Longevity Sciences, National Center for Geriatrics and Gerontology, Obu, Japan [3] Department of Pathology and Applied Neurobiology, Graduate School of Medical Science, Kyoto Prefectural University of Mediciene, Kyoto, Japan

Background: TARSH (Target of NESH-SH3) is a presumptive signal transduction molecule interacting with NESH which is implicated to have some roles in lung cancer metastasis. We have previously found evidence for TARSH being predominantly expressed in the mouse lung and being induced during cellular senescence of mouse embryonic fibroblasts. On the basis of relationship between cellular senescence and carcinogenesis, we analyzed TARSH mRNA expression in human primary lung cancer.

Methods: Fifteen human lung cancer cell lines and 80 clinical cancer specimens were analyzed in this study. Both neoplastic and non-neoplastic tissue samples were obtained from patients who underwent surgery for primary lung cancer: 58 for adenocarcinoma including 10 of bronchioloalveolar carcinoma (BAC), 17 for squamous cell carcinoma, and 5 for the others (including 3 of large cell carcinoma and 2 of small cell carcinoma). Total RNA was extracted from each sample, followed by quantitative real-time reverse transcription PCR with SYBR Green. The expression level of TARSH in each sample was normalized with respect to that of GAPDH. We then defined T/N ratio as the ratio of the average mRNA expression levels for each clinical cancer specimen to that of corresponding non-neoplastic lung tissue.

Results: On the Northern hybridization analysis, TARSH was strongly expressed in the human normal lung. In 15 human lung cancer cell lines tested, TARSH expression was completely lost or remarkably down-regulated as demonstrated by quantitative real-time RT-PCR. We found that TARSH expression level was reduced in all cancer specimens when compared with the non-neoplastic lung tissue obtained from the same patient. The T/N ratio in adenocarcinoma, squamous cell carcinoma and the others was 0.126 (in a range from 0.003 to 0.832), 0.011 (from 0.001 to 0.035) and 0.072 (from 0.001 to 0.231) respectively. In particular, BAC showed relatively higher T/N ratio than others. There was some correlation between TARSH expression and clinicopathological characteristics when applied multi-parametric analysis.

Conclusions: The expression of TARSH mRNA was remarkably downregulated in all lung cancer cell lines examined, and significantly low in all (80 cases) of the lung cancer specimens when compared to the expression in corresponding non-neoplastic lung tissue specimens. The cancer-associated transcriptional inactivation of TARSH suggests that TARSH could be used as a biomarker for lung cancer development.

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